

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 12:31:02 ; Search time 2024.2 seconds
(without alignments)
3615.194 Million cell updates/sec

Title: US-09-602-833A-3
Perfect score: 681
Sequence: 1 atgaatactcgcattgcgc.....ctttagccttcaacttga 681

Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*
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2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gp_est1:*
11: gp_est2:*
12: gp_hic:*
13: gp_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	20.3	370	11	BG197958 RST17210
2	138	20.3	377	11	BG203142 RST32516
3	137	20.1	598	13	AO670712 HS_5449_A
4	126	18.5	508	11	BG210970 RST30524
5	125	18.4	470	10	AL120256 DKFP761J
6	125	18.4	669	10	AL133928 DKFP761O
7	64	9.4	377	10	AI399758 t963a12.x
8	46	6.8	298	11	BF840611 MRI-HT106
9	38	5.6	483	10	AA422330 VF45B09.T
10	38	5.6	526	10	AA416235 VF38B07.T
11	38	5.6	1450	12	AK010252 Mus muscu
12	34	5.0	377	11	BF839187 MRI-HT106

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	COMMENT	FEATURES
1	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
2	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
3	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
4	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
5	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
6	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
7	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
8	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
9	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
10	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
11	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
12	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
13	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
14	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
15	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
16	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
17	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
18	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
19	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
20	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
21	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
22	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
23	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
24	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
25	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
26	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
27	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
28	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
29	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
30	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
31	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
32	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
33	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
34	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
35	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
36	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
37	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
38	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
39	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
40	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
41	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
42	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
43	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
44	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370
45	BG197958	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	human.	Homo sapiens	Activation of Gene Expression	Nat. Biotechnol. 19 (5), 440 (2001) In press	Contact: Scott J. Cain	1. .370

ALIGNMENTS

RESULT 1
LOCUS BG197958 370 bp mRNA
DEFINITION RST17210 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
ACCESSION BG197958
VERSION BG197958.1 GI:13719645
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 370)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, U., Lerner, L., Krishoc, D., McElligott, K., Clark, S., Mays, R., Smith, E., Veloso, N., Hess, J., Colthen, K., Lo, K., Offenbacher, J., Danzig, J., and Ducar, M.
Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression
Nat. Biotechnol. 19 (5), 440 (2001) In press
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 324.
Location/Qualifiers
1. .370
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression',

Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

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137 a 65 c 63 g 104 t 1 others

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Best Local Similarity 100.0%; Pred. No. 6,6e-62;
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DB 48 GGCAATGAATAATGGAAGTGAACGGATGCCAATTTTGATTAAGAGTTATGAAA 107
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OY 604 gccatattgaagacctaaagaagatcgttccacgtatcacccaagtgtct 663
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DB 108 GCCATATTGAAGACTTAAAGAAAGAAATCTGTCCAGCTATACCAACAAGTGCT 167
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OY 664 tttagcctcaacttga 681
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DB 168 TTTAGCCTTCAACTTGA 185
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RESULT 2
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LOCUS RST22516 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION BG203142
ACCESSION BG203142
VERSION BG203142.1 GI:13724829
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E., Veloso,N., Hess,J., Colhren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

TITLE Creation of Genome-wide Protein Expression Libraries using Random
JOURNAL Activation of Gene Expression
COMMENT Nat. Biotechnol. 19 (5), 440 (2001) In press
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com

FEATURES
source High quality sequence stop: 377.
Location/Qualifiers
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OY 544 ggcaatgaataatggaagtgacggatgcacacatttgataagaagtatgaa 603

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OY 604 gccatattgaagacctaaagaagatcgttccacgtatcacccaagtgtct 663
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OY 664 tttagcctcaacttga 681
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DB 174 TTTAGCCTTCAACTTGA 191
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RESULT 3
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DEFINITION genomic clone Plate-1025 Col-22 Row-I, DNA sequence.
ACCESSION A0670712
VERSION A0670712.1 GI:5203458
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
COMMENT 99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@edlong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1025 row: I column: 22
Seq primer: T7
Class: BAC ends

FEATURES
source High quality sequence stop: 598.
Location/Qualifiers
1..598

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BASE COUNT 185 a 97 c 121 g 187 t 8 others
ORIGIN

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Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 615 agacctaaagaagaag 631
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Db 303 AGACCTTAAGAAGAAG 319

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DEFINITION R3130524 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION Bg210970
VERSION Bg210970.1 GI:13732657
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E.,
Velooso,N., Hess,J., Colhren,K., Lo,K., Offenbacher,J., Danzig,J.
and Ducar,M.
TITLE Creation of Genome-wide Protein Expression Libraries using Random
JOURNAL Activation of Gene Expression
COMMENT Nat. Biotechnol. 19 (5), 440 (2001) In press
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave., Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaine@atersys.com
BASE COUNT 182 a 81 c 83 g 160 t
ORIGIN
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1. 508
/organism="Homo sapiens"
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/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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QY 616 gacctaaagaagaagtatctgtccagctataccacaaagtctctttagccttca 675
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Db 125 GACCTTAAGAAGAAGATCTGTCCAGCTATACCAACAAAGTGCTTTTAGCCTTCA 184
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QY 676 cttga 681
      |||||||
Db 185 CTTTGA 190

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LOCUS AL120256
DEFINITION DKFp761J017_t1 761 (synonym: hamy2) Homo sapiens cDNA clone

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ACCESSION DKFp761J017 5', mRNA sequence.
AL120256
VERSION AL120256.1 GI:5926155
KEYWORDS EST.
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehler, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Koehler K
MPS
Am Kiopterapitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No 5' sequence available.
This clone (DKFp761J017) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
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1. 470
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Best Local Similarity 100.0%; Pred. No. 5e-55;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 tggaaagtgaacggatcgccaacatttgataaagaagtatagaagcctatatga 616
      |||||||
Db 1 TGGAAAGTGAACGGATCGCCAACATTTGATTAAGAAGTATATGAACCTATATTAAG 60
      |||||||
QY 617 accttaagaagaagaatctgttccagctataccacaaagtctctttagccttca 676
      |||||||
Db 61 ACCTTAAGAAGAAGATCTGTCCAGCTATACCAACAAAGTGCTTTAGCCTTCAAC 120
      |||||||
QY 677 tttga 681
      |||||||
Db 121 TTTGA 125

RESULT 6
AL133928
LOCUS AL133928
DEFINITION DKFp761O1814_t1 761 (synonym: hamy2) Homo sapiens cDNA clone
ACCESSION DKFp761O1814 5', mRNA sequence.
AL133928
VERSION AL133928.1 GI:6602115
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ansoerge,W., Wirtner,U., Mewes,H.W., Well,B. and Wiemann,S.
TITLE EST (Ansoerge,W., Wirtner,U., Mewes,H.W., Well,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: Ansoerge W

```

MIPS
Am Klopferplatz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZ76101814) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers

BASE COUNT 214 a 118 c 141 g 196 t
ORIGIN
1. .669
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZ76101814"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

Query Match 18.4%; Score 125; DB 10; Length 669;

Best Local Similarity 100.0%; Pred. No. 5.1e-55;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 557 tggaaatgaaagcggatgcgaacatttgataaagaagttaagaagccatattgaag 616
|||||
Db 1 TGGAAAGTGAACGGGATCGCCACATTTTGAATAAGAGTATGAAACCTATATGGAAG 60
Y 617 acctaaagaagaagatctgtcccgactacaccagaagctctttaagccttaaac 676
|||||
Db 61 ACCTTAAGAAGAAGATCTGTCTCCAGCTATACCAACCAAGTGTCTTTAGCCTTCAC 120
Y 677 ttga 681
|||||
Db 121 TTGCA 125

RESULT 7
AI399758 377 bp mRNA EST 30-MAR-1999
LOCUS
DEFINITION
t963a12.x1 Soares_NhMpu_S1 Homo sapiens cDNA clone IMAGE:2113438
3', mRNA sequence.
ACCESSION
AI399758
VERSION
AI399758.1 GI:4242845
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 377)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-f@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 675 Std Error: 0.00
Seq primer: -400P from G1bco
High quality sequence stop: 363.
Location/Qualifiers

FEATURES

1. .377
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2113438"
/clone_lib="Soares_NhMpu_S1"

/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pRT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI. Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbM, pregnant uterus
NbHpu, and fetal heart NbH19w) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT 129 a 55 c 63 g 130 t
ORIGIN

Query Match 9.4%; Score 64; DB 10; Length 377;

Best Local Similarity 100.0%; Pred. No. 9e-23;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 618 ccttaagaagaagatctgtcccgactacaccagaagctctttaagccttaaac 677
|||||
Db 377 CCTTAAGAAGAAGATCTGTCTCCAGCTATACCAACCAAGTGTCTTTAGCCTTCAC 318
Y 678 ttga 681
|||||
Db 317 TTGCA 314

RESULT 8
BF840611 298 bp mRNA EST 13-JAN-2001
LOCUS
DEFINITION
MRL-HT1068-011200-006-a06 HT1068 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF840611
VERSION
BF840611.1 GI:12193121
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 298)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR1&t2=MRI-HT1068-
011200-006-a06&t3=2000-12-01&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 298.
Location/Qualifiers

FEATURES

1. .298
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT1068"

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/dev_stage="adult"
/note="Organ: head, neck; Vector: puc18; Site: 1; SmaI:
Site: 2; SmaI: A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      94 a      59 c      51 g      94 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 46; DB 11; Length 298;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 ttctctgtataaaacaaagtgaacctaccctcctatccatgcct 404
Db 241 TTCTCTGTATATAAACAGTTGACCTACCTCCCTATTCATCT 286

RESULT 9
LOCUS AA422330 483 bp mRNA EST 16-OCT-1997
DEFINITION vF45D09.r1 Soares mouse NbMH Mus musculus cDNA clone IMAGE:846713
5' similar to TR:G440177 G440177 HOMOLOG OF D. MELANOGASTER
FLIGHTLESS-1 GENE PRODUCT ;, mRNA sequence.
ACCESSION AA422330
VERSION AA422330.1 GI:2101146
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
1 (bases 1 to 483)
REFERENCE 1
AUTHORS Mairia, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Mairia M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:498865
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 479.
Location/Qualifiers
1. 483
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:846713"
/clone_lib="Soares mouse NbMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATTCGAGTGGAGCGCGGAGGATTTTGTGTGTGTGTGTGTGTGT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Minoru Ko, Wayne State Univ. Library

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constructed and normalized by Bento Soares and M. Fatima
Bonaldo."
BASE COUNT      125 a      115 c      120 g      123 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 38; DB 10; Length 483;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 cccttgaattgaattgaagcaagttacattgt 221
Db 99 CCCTTGAAATTAAGTAATTGACCAAGTACATTGT 136

RESULT 10
LOCUS AA416235 526 bp mRNA EST 16-OCT-1997
DEFINITION vF38D07.r1 Soares mouse NbMH Mus musculus cDNA clone IMAGE:846037
5' similar to TR:G440177 G440177 HOMOLOG OF D. MELANOGASTER
FLIGHTLESS-1 GENE PRODUCT ;, mRNA sequence.
ACCESSION AA416235
VERSION AA416235.1 GI:2076503
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
1 (bases 1 to 526)
REFERENCE 1
AUTHORS Mairia, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Mairia M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:498189
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 482.
Location/Qualifiers
1. 526
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:846037"
/clone_lib="Soares mouse NbMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATTCGAGTGGAGCGCGGAGGATTTTGTGTGTGTGTGTGTGTGT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."
BASE COUNT      140 a      122 c      130 g      134 t
ORIGIN

```


COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR1&t2=MR1-H71068-
281100-004-d12&t3=2000-11-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 341.
Location/Qualifiers
1. 377
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="H71068"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 112 a 71 c 89 g 105 t
ORIGIN

Query Match 5.0%; Score 34; DB 11; Length 377;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 365 tctataaacaagttgacctactcctcctatc 398
Db 344 TGTATAAACAACTGACCTACTCCTCCTATTC 377

RESULT 13
AQ427288/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AQ427288 560 bp DNA GSS 24-MAR-1999
CITR1-E1-2568D1.TR CITR1-E1 Homo sapiens genomic clone 2568D1, DNA
sequence.
AQ427288
GSS.
AQ427288.1 GI:4500038
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 560)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Other_GSSs: CITR1-E1-2568D1.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers

FEATURES
source

source 1. 560
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2568D1"
/clone_id="CITR1-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC library D"

BASE COUNT 132 a 154 c 101 g 173 t
ORIGIN

Query Match 4.6%; Score 31; DB 13; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 gttcaactatctgaagacatctcctcaga 119
Db 79 GTTCACTATCTGAGACATCTCCTCAGA 49

RESULT 14
AQ427239/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AQ427239 572 bp DNA GSS 24-MAR-1999
CITR1-E1-2568B9.TR CITR1-E1 Homo sapiens genomic clone 2568B9, DNA
sequence.
AQ427239
GSS.
AQ427239.1 GI:4499942
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 572)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Other_GSSs: CITR1-E1-2568B9.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers

FEATURES
source

1. 572
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2568B9"
/clone_id="CITR1-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC library D"

BASE COUNT 134 a 157 c 104 g 177 t
ORIGIN

Query Match 4.6%; Score 31; DB 13; Length 572;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 gttcaactatctgaagacatctcctcaga 119
|||||

Db 79 GTTCACTATCTGAAGACATTCCTCCAGA 49

RESULT 15

LOCUS AI561877

DEFINITION VJ48d03.X1 Stratiagene mouse heart (#937316) Mus musculus cDNA clone

ACCESSION AI561877

VERSION AI561877.1 GI:4513222

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE

AUTHORS

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritzer,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)

TITLE JOURNAL

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:537181

This clone was previously sequenced on the 5' end only, this new data is from the 3' end
High quality sequence stop: 300.

FEATURES

source

location/Qualifiers

1..319

/organism="Mus musculus"

/strain="NIH/5Wiss"

/db_xref="taxon:10090"

/clone="IMAGE:932261"

/clone_lib="Stratiagene mouse heart (#937316)"

/sex="pooled"

/tissue_type="heart"

/dev_stage="13 day embryos"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: heart; Vector: pBluescript SK-; Site:1: EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo df: 93 pooled NIH/5Wiss 13 day embryo hearts"

Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'

adaptor sequence: 5' GAATTCGGCAGCGAG 3' -3' adaptor

sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'

BASE COUNT 82 a 74 c 74 g 89 t

ORIGIN

Query Match

Best Local Similarity 4.3%; Score 29; DB 10; Length 319;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 ttaagtaattgaagcaagttacattgt 221
|||||
Db 271 TTAAGTAATTGAAGCAAGTTACATTGT 299

Search completed: February 26, 2002, 12:31:04
Job time: 6390 sec